P-8. A selection model taking the magnitude and the gene frequency of loci into account(Abstracts of the International Symposium on Recent Advances in Animal Science(IS-RAAS),Joint meeting of 2^<nd> IS-AS and 3^<rd> IS-IFS)

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journal or publication title	Tohoku journal of agricultural research
volume	56
number	1/2
page range	39-39
year	2005-11-25
URL	http://hdl.handle.net/10097/30089

P-7. A comparison of restricted selection procedures to control genetic gains

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Using Monte Carlo simulation, two schemes of restricted selection were compared under various combinations of genetic parameters and constraints on the genetic gains. The first selection scheme is the combination of BLUP evaluation and linear programming technique (BLUP+LP), and the second one is based on the restricted BLUP selection (RBLUP). Selection for two traits was supposed, in which animals were selected to maximize the genetic gain in trait 2 ($\Delta G2$) under a proportional restriction on the genetic gain in trait 1 ($\Delta G1$) to satisfy the intended ratio ($\Delta G1$: $\Delta G2$). Little differences were found between the two selection schemes with respect to the genetic gains averaged over replicates. However, in all the cases studied, the variance of genetic gains among replicates under BLUP+LP selection was smaller and less sensitive to the genetic parameters and the intended restriction than RBLUP selection. Under the situations of antagonistic selection, the difference tended to be larger. When the heritabilities of the two traits were different, RBLUP selection remarkably increased the variance of genetic gain in a trait with a higher heritability. These results suggest that BLUP+LP selection should always be preferable to RBLUP selection because of the smaller risk of selection. This choice is especially important for the situation where the genetic parameters act as limiting factors for the achievement of intended genetic gains.

P-8. A selection model taking the magnitude and the gene frequency of loci into account

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We show a procedure of calculating genetic change taking the magnitude and the gene frequency of loci into account. The calculating procedure is tracing the gene frequency and the difference of the expected effect on the other loci between gametes having desirable and opposite allele on each locus.

The covariance among loci, Bulmer effect, is usually considered as halved every generation. It is expired when the selected heterozygote segregates, and is halved only when the rate of heterozygote agree with the Hardy-Weinberg proportion. The accumulated change of genetic variance is much affected by the gene frequency, since the recovery of the variance due to segregation and the genetic gain are different. Even when start with the same initial variance, initial gene frequencies and the selection limit, the model with various magnitude of loci shows faster reduction on genetic variance, because of the faster reduction in loci of large effect.

It is indicated that the prediction of the genetic change leaving the magnitude and the gene frequency of loci out of accounts have risk of discrepancy especially when relatively large loci exist.